

SEQUENCE LISTING

- 5 SEQ ID NO: 1 is mouse TECK nucleotide sequence.
SEQ ID NO: 2 is mouse TECK amino acid sequence.
SEQ ID NO: 3 is human TECK nucleotide sequence.
SEQ ID NO: 4 is human TECK amino acid sequence.
SEQ ID NO: 5 is human MIP-3 α nucleotide sequence.
10 SEQ ID NO: 6 is human MIP-3 α amino acid sequence.
SEQ ID NO: 7 is human MIP-3 β nucleotide sequence.
SEQ ID NO: 8 is human MIP-3 β amino acid sequence.
SEQ ID NO: 9 is human DC CR nucleotide sequence.
SEQ ID NO: 10 is human DC CR amino acid sequence.
15 SEQ ID NO: 11 is human M/DC CR nucleotide sequence.
SEQ ID NO: 12 is human M/DC CR amino acid sequence.
SEQ ID NO: 13 is human CCKR1 amino acid sequence.
SEQ ID NO: 14 is human CCKR2 amino acid sequence.
SEQ ID NO: 15 is human CCKR3 amino acid sequence.
20 SEQ ID NO: 16 is human CCKR4 amino acid sequence.
SEQ ID NO: 17 is HPRT sense primer.
SEQ ID NO: 18 is HPRT antisense primer.
SEQ ID NO: 19 is FLAG epitope tag sequence.
- 25 (1) GENERAL INFORMATION:
- (i) APPLICANT: Wang, Wei
Gish, Kurt C.
Schall, Thomas J.
30 Vicari, Alain P.
Zlotnik, Albert
- (ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
- 35 (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
40 (C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104
- 45 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 50 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 55 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/675,814
(B) FILING DATE: 05-JUL-1996
- 60 provisional filings DX0589P, DX0589P1; DX0589P2

various

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: DX0589Q1

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 94..525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

30 AGGCTACAAG CAGGCACCAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT 60
TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC 114
Met Lys Leu Trp Leu Phe Ala
1 5
35 TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC 162
Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala
10 15 20
40 CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA 210
Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys
25 30 35
45 TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT 258
Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser
40 45 50 55
50 GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA 306
Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val
60 65 70
55 GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC 354
Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile
75 80 85
60 TTG ACA GCT AGG AAA AGG CTA GTC CAC TGG AAG AGC GCC TCA GAC TCT 402
Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser
90 95 100
60 CAG ACT GAA AGG AAG AAG TCA AAC CAT ATG AAG TCC AAG GTG GAG AAC 450

Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn
 105 110 115

5 CCC AAC AGT ACA AGC GTG AGG AGT GCC ACC CTA GGT CAT CCC AGG ATG 498
 Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met
 120 125 130 135

10 GTG ATG ATG CCC AGA AAG ACC AAC AAT TAAGTTAATT ACTCAGAGTA 545
 Val Met Met Pro Arg Lys Thr Asn Asn
 140

AGCACCAGCT GGAGGATGGG CGGAGTCTGC TGAAGTGCTG TCTTCTAGGC ATGCCAGTGC 605

15 CAATGAACTC ACTGAAGCTA CAGTTTCCTG TACAAGACCA GACCCACCAA CGTCTCAGCA 665
 TGTACGAGGA AGGAACTACT GCGCTAAAGG CCCTCCCACT CACCAAGGAG CTATTGGCTA 725
 TTGATGATTG CTGAGGGAAG GGAGTAATTT TTTTCTCTT TCTGAAGTGT GACTTGAGTA 785

20 AATTGCCCAT AGTTCAGTAT ATAATCCCCA ACCTGTGCTC AGGCAAGCAA CCCTAATTAA 845
 ATGCAATAGC CACATACAAA AGAAGAGGAT ATGAATAGTT TGGTAGGAGG GGCTTGTTAG 905
 GAAGAAGACA TTAACAGGAG AGAGAGGAGC GAGAGGATAG TGAGTGTGTG AGAGTGCCTG 965

25 CACGTGTGAA ATGGTCAAAG AATTAAAAAA TAAAACTTA AAAAGCTATT AAAAAGTAAA 1025
 AAAAATAAA 1034

30 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 35 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Trp Leu Phe Ala Cys Leu Val Ala Cys Phe Val Gly Ala
 1 5 10 15

45 Trp Met Pro Val Val His Ala Gln Gly Ala Phe Glu Asp Cys Cys Leu
 20 25 30

Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn
 35 40 45

50 Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg
 50 55 60

55 Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
 65 70 75 80

Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
 85 90 95

60 Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His

100 105 110

Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
115 120 125

5 Thr Leu Gly His Pro Arg Met Val Met Met Pro Arg Lys Thr Asn Asn
130 135 140

10 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1012 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 117..566

25 (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 186..566

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCGGGCAT CAGCTCCCTT GACCCAGTGG 60

ATATCGGTGG CCCCGTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC 116

35 ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC 164
Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
-23 -20 -15 -10

40 TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG 212
Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
-5 1 5

GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT 260

45 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr 25
10 15 20 25

TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA 308

50 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile 40
30 35 40

TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC 356

Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser 55
45 50 55

55 AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT 404
Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
60 65 70

60 TTT GCA AAG CTC CAC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT 452

Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
 75 80 85

5 GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG 500
 Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
 90 95 100 105

10 TTT AGC AAT CCC ATC AGC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA 548
 Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
 110 115 120

15 TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTTCTGGG CTCCATCGGC 596
 Ser Ala Asn Ser Gly Leu
 125

ACAGGAGGGG CCGGATCTTT CTCCGATAAA ACCGTCGCCC TACAGACCCA GCTGTCCCCA 656

CGCCTCTGTC TTTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCCT CCCTCTGCAC 716

20 CCCCACCACC TCCTGCCCCGT CTGGCAACTG GAAAGAAGGA GTTGGCCTGA TTTTAACCTT 776

TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGTAG AGAAAACTTA 836

25 GGATACCTCT CTCACCTTCT GTTTCTTGCC GTCCACCCCG GGCCATGCCA GTGTGTCTTC 896

TGGGTCCCCT CCAAAAATCT GGTCAATCAA GGATCCCCTC CCAAGGCTAT GCTTTTCTAT 956

AACTTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAAAA AAAAAA 1012

30

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 150 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
 -23 -20 -15 -10

45 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
 -5 1 5

Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
 10 15 20 25

50 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
 30 35 40

55 Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
 45 50 55

Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
 60 65 70

60 Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His

75 80 85

Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
 90 95 100 105

5 Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
 110 115 120

Ser Ala Asn Ser Gly Leu
 10 125

(2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 25 (A) NAME/KEY: CDS
 (B) LOCATION: 1..288

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 79..288

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35 ATG TGC TGT ACC AAG AGT TTG CTC CTG GCT GCT TTG ATG TCA GTG CTG 48
 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 -26 -25 -20 -15

40 CTA CTC CAC CTC TGC GGC GAA TCA GAA GCA GCA AGC AAC TTT GAC TGC 96
 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 -10 -5 1 5

TGT CTT GGA TAC ACA GAC CGT ATT CTT CAT CCT AAA TTT ATT GTG GGC 144
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20

45 TTC ACA CGG CAG CTG GCC AAT GAA GGC TGT GAC ATC AAT GCT ATC ATC 192
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35

50 TTT CAC ACA AAG AAA AAG TTG TCT GTG TGC GCA AAT CCA AAA CAG ACT 240
 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50

55 TGG GTG AAA TAT ATT GTG CGT CTC CTC AGT AAA AAA GTC AAG AAC ATG 288
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70

TAAAACTGT GGCTTTTCTG GAATGGAATT GGACATAGCC CAAGAACAGA AAGAACCTTG 348

60 CTGGGGTTGG AGGTTTCACT TGCACATCAT GGAGGGTTTA GTGCTTATCT AATTTGTGCC 408

TCACTGGACT TGTCCAATTA ATGAAGTTGA TTCATATTGC ATCATAGTTT GCTTTGTTTA 468
 AGCATCACAT TAAAGTTAAA CTGTATTTTA TGTTATTTAT AGCTGTAGGT TTTCTGTGTT 528
 5 TAGCTATTTA ATACTAATTT TCCATAAGCT ATTTTGGTTT AGTGCAAAGT ATAAAATTAT 588
 ATTTGGGGGG GAATAAGATT ATATGGACTT TTTTGCAAGC AACAAGCTAT TTTTAAAAA 648
 10 AACTATTTA ACATTCTTTT GTTTATATTG TTTGTCTCC TAAATTGTTG TAATTGCATT 708
 ATAAAATAAG AAAAATATTA ATAAGACAAA TATTGAAAAT AAAGAAACAA AAAGTTAAAA 768
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 801
 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
 -26 -25 -20 -15
 30 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 -10 -5 1 5
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 35 10 15 20
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 40 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70
 45

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 699 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

60 (A) NAME/KEY: CDS
 (B) LOCATION: 142..435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 GGCACGAGCG GCACGAGCAT CACTCACACC TTGCATTTCA CCCCTGCATC CCAGTCGCCC 60
 TGCAGCCTCA CACAGATCCT GCACACACCC AGACAGCTGG CGCTCACACA TTCACCGTTG 120
 GCCTGCCTCT GTTCACCCTC C ATG GCC CTG CTA CTG GCC CTC AGC CTG CTG 171
 10 Met Ala Leu Leu Leu Ala Leu Ser Leu Leu
 1 5 10
 GTT CTC TGG ACT TCC CCA GCC CCA ACT CTG AGT GGC ACC AAT GAT GCT 219
 15 Val Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala
 15 20 25
 GAA GAC TGC TGC CTG TCT GTG ACC CAG AAA CCC ATC CCT GGG TAC ATC 267
 Glu Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile
 30 35 40
 20 GTG AGG AAC TTC CAC TAC CTT CTC ATC AAG GAT GGC TGC AGG GTG CCT 315
 Val Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro
 45 50 55
 25 GCT GTA GTG TTC ACC ACA CTG AGG GGC CGC CAG CTC TGT GCA CCC CCA 363
 Ala Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro
 60 65 70
 30 GAC CAG CCC TGG GTA GAA CGC ATC ATC CAG AGA CTG CAG AGG ACC TCA 411
 Asp Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser
 75 80 85 90
 GCC AAG ATG AAG CGC CGC AGC AGT TAACCTATGA CCGTGCAGAG GGAGCCCCGA 465
 35 Ala Lys Met Lys Arg Arg Ser Ser
 95
 GTCCGAGTCA AGCATTGTGA ATTATTACCT AACCTGGGGA ACCGAGGACC AGAAGGAAGG 525
 ACCAGGCTTC CAGCTCCTCT GCACCAGACC TGACCAGCCA GGACAGGGCC TGGGGTGTGT 585
 40 GTGAGTGTGA GTGTGAGCGA GAGGGTGAGT GTGGTCTAGA GTAAAGCTGC TCCACCCCCA 645
 GATTGCAATG CTACCAATAA AGCCGCCTGG TGTTTACAAC TAAAAA AAAA 699

45

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
 1 5 10 15
 60 Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser

		20		25		30	
	Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr						
		35		40		45	
5	Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr						
		50		55		60	
10	Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu						
		65		70		75	
	Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Arg Arg						
			85		90		95
15	Ser Ser						

(2) INFORMATION FOR SEQ ID NO:9:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

30 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1095

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

35	ATG TTT TCG ACT CCA GTG AAG ATT ATT TTG TGT CAG TCA ATA CTT CAT	48
	Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His	
	1 5 10 15	
40	ATT ACT CAG TTG ATT CTG AGA TGT TAC TGT GCT CCT TGC AGG AGG TCA	96
	Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser	
	20 25 30	
45	GGC AGT TCT CCA GGC TAT TTG TAC CGA ATT GCC TAC TCC TTG ATC TGT	144
	Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys	
	35 40 45	
50	GTT CTT GGC CTC CTG GGG AAT ATT CTG GTG GTG ATC ACC TTT GCT TTT	192
	Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe	
	50 55 60	
55	TAT AAG AAG GCC AGG TCT ATG ACA GAC GTC TAT CTC TTG AAC ATG GCC	240
	Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala	
	65 70 75 80	
60	ATT GCA GAC ATC CTC TTT GTT CTT ACT CTC CCA TTC TGG GCA GTG AGT	288
	Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser	
	85 90 95	
60	CAT GCC ACT GGT GCG TGG GTT TTC AGC AAT GCC ACG TGC AAG TTG CTA	336

	His	Ala	Thr	Gly	Ala	Trp	Val	Phe	Ser	Asn	Ala	Thr	Cys	Lys	Leu	Leu	
				100					105					110			
5	AAA	GGC	ATC	TAT	GCC	ATC	AAC	TTT	AAC	TGC	GGG	ATG	CTG	CTC	CTG	ACT	384
	Lys	Gly	Ile	Tyr	Ala	Ile	Asn	Phe	Asn	Cys	Gly	Met	Leu	Leu	Leu	Thr	
			115					120					125				
10	TGC	ATT	AGC	ATG	GAC	CGG	TAC	ATC	GCC	ATT	GTA	CAG	GCG	ACT	AAG	TCA	432
	Cys	Ile	Ser	Met	Asp	Arg	Tyr	Ile	Ala	Ile	Val	Gln	Ala	Thr	Lys	Ser	
			130				135					140					
15	TTC	CGG	CTC	CGA	TCC	AGA	ACA	CTA	CCG	CGC	AGC	AAA	ATC	ATC	TGC	CTT	480
	Phe	Arg	Leu	Arg	Ser	Arg	Thr	Leu	Pro	Arg	Ser	Lys	Ile	Ile	Cys	Leu	
						150					155					160	
	GTT	GTG	TGG	GGG	CTG	TCA	GTC	ATC	ATC	TCC	AGC	TCA	ACT	TTT	GTC	TTC	528
	Val	Val	Trp	Gly	Leu	Ser	Val	Ile	Ile	Ser	Ser	Ser	Thr	Phe	Val	Phe	
					165					170					175		
20	AAC	CAA	AAA	TAC	AAC	ACC	CAA	GGC	AGC	GAT	GTC	TGT	GAA	CCC	AAG	TAC	576
	Asn	Gln	Lys	Tyr	Asn	Thr	Gln	Gly	Ser	Asp	Val	Cys	Glu	Pro	Lys	Tyr	
				180					185					190			
25	CAA	ACT	GTC	TCG	GAG	CCC	ATC	AGG	TGG	AAG	CTG	CTG	ATG	TTG	GGG	CTT	624
	Gln	Thr	Val	Ser	Glu	Pro	Ile	Arg	Trp	Lys	Leu	Leu	Met	Leu	Gly	Leu	
			195					200					205				
30	GAG	CTA	CTC	TTT	GGT	TTC	TTT	ATC	CCT	TTG	ATG	TTC	ATG	ATA	TTT	TGT	672
	Glu	Leu	Leu	Phe	Gly	Phe	Phe	Ile	Pro	Leu	Met	Phe	Met	Ile	Phe	Cys	
		210					215					220					
35	TAC	ACG	TTC	ATT	GTC	AAA	ACC	TTG	GTG	CAA	GCT	CAG	AAT	TCT	AAA	AGG	720
	Tyr	Thr	Phe	Ile	Val	Lys	Thr	Leu	Val	Gln	Ala	Gln	Asn	Ser	Lys	Arg	
						230					235					240	
	CAC	AAA	GCC	ATC	CGT	GTA	ATC	ATA	GCT	GTG	GTG	CTT	GTG	TTT	CTG	GCT	768
	His	Lys	Ala	Ile	Arg	Val	Ile	Ile	Ala	Val	Val	Leu	Val	Phe	Leu	Ala	
					245					250					255		
40	TGT	CAG	ATT	CCT	CAT	AAC	ATG	GTC	CTG	CTT	GTG	ACG	GCT	GCT	AAT	TTG	816
	Cys	Gln	Ile	Pro	His	Asn	Met	Val	Leu	Leu	Val	Thr	Ala	Ala	Asn	Leu	
				260					265					270			
45	GGT	AAA	ATG	AAC	CGA	TCC	TGC	CAG	AGC	GAA	AAG	CTA	ATT	GGC	TAT	ACG	864
	Gly	Lys	Met	Asn	Arg	Ser	Cys	Gln	Ser	Glu	Lys	Leu	Ile	Gly	Tyr	Thr	
			275					280					285				
50	AAA	ACT	GTC	ACA	GAA	GTC	CTG	GCT	TTC	CTG	CAC	TGC	TGC	CTG	AAC	CCT	912
	Lys	Thr	Val	Thr	Glu	Val	Leu	Ala	Phe	Leu	His	Cys	Cys	Leu	Asn	Pro	
			290				295					300					
55	GTG	CTC	TAC	GCT	TTT	ATT	GGG	CAG	AAG	TTC	AGA	AAC	TAC	TTT	CTG	AAG	960
	Val	Leu	Tyr	Ala	Phe	Ile	Gly	Gln	Lys	Phe	Arg	Asn	Tyr	Phe	Leu	Lys	
		305				310					315					320	
	ATC	TTG	AAG	GAC	CTG	TGG	TGT	GTG	AGA	AGG	AAG	TAC	AAG	TCC	TCA	GGC	1008
	Ile	Leu	Lys	Asp	Leu	Trp	Cys	Val	Arg	Arg	Lys	Tyr	Lys	Ser	Ser	Gly	
					325					330					335		
60	TTC	TCC	TGT	GCC	GGG	AGG	TAC	TCA	GAA	AAC	ATT	TCT	CGG	CAG	ACC	AGT	1056

Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser
 340 345 350

5 GAG ACC GCA GAT AAC GAC AAT GCG TCG TCC TTC ACT ATG TGATAGAAAG 1105
 Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met
 355 360 365

CTGAGTCTCC CTAA 1119

10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Ser Thr Pro Val Lys Ile Ile Leu Cys Gln Ser Ile Leu His
 1 5 10 15
 25 Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser
 20 25 30
 Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
 35 40 45
 30 Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
 50 55 60
 35 Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
 65 70 75 80
 Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser
 85 90 95
 40 His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu
 100 105 110
 Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr
 115 120 125
 45 Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
 130 135 140
 Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu
 145 150 155 160
 Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe
 165 170 175
 55 Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr
 180 185 190
 Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu
 195 200 205

60

Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys
 210 215 220
 Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg
 5 225 230 235 240
 His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala
 245 250 255
 10 Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu
 260 265 270
 Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr
 275 280 285
 15 Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro
 290 295 300
 Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys
 20 305 310 315 320
 Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly
 325 330 335
 25 Phe Ser Cys Ala Gly Arg Tyr Ser Glu Asn Ile Ser Arg Gln Thr Ser
 340 345 350
 Glu Thr Ala Asp Asn Asp Asn Ala Ser Ser Phe Thr Met
 355 360 365
 30

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40

(ix) FEATURE:

- 45 (A) NAME/KEY: CDS
 (B) LOCATION: 49..1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50 GAGGAAGCTG CTCGGGGGGG TGAGCAAAC TTTTAAAATG CAGAAATT ATG ATC TAC 57
 Met Ile Tyr
 1
 ACC CGT TTC TTA AAA GGC AGT CTG AAG ATG GCC AAT TAC ACG CTG GCA 105
 Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr Thr Leu Ala
 5 10 15
 CCA GAG GAT GAA TAT GAT GTC CTC ATA GAA GGT GAA CTG GAG AGC GAT 153
 Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp
 20 25 30 35
 60

	GAG GCA GAG CAA TGT GAC AAG TAT GAC GCC CAG GCA CTC TCA GCC CAG	201
	Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln	
	40 45 50	
5	CTG GTG CCA TCA CTC TGC TCT GCT GTG TTT GTG ATC GGT GTC CTG GAC	249
	Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp	
	55 60 65	
10	AAT CTC CTG GTT GTG CTT ATC CTG GTA AAA TAT AAA GGA CTC AAA CGC	297
	Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg	
	70 75 80	
15	GTG GAA AAT ATC TAT CTT CTA AAC TTG GCA GTT TCT AAC TTG TGT TTC	345
	Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe	
	85 90 95	
20	TTG CTT ACC CTG CCC TTC TGG GCT CAT GCT GGG GGC GAT CCC ATG TGT	393
	Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys	
	100 105 110 115	
	AAA ATT CTC ATT GGA CTG TAC TTC GTG GGC CTG TAC AGT GAG ACA TTT	441
	Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe	
	120 125 130	
25	TTC AAT TGC CTT CTG ACT GTG CAA AGG TAC CTA GTG TTT TTG CAC AAG	489
	Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe Leu His Lys	
	135 140 145	
30	GGC AAC TTT TTC TCA GCC AGG AGG AGG GTG CCC TGT GGC ATC ATT ACA	537
	Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Ile Thr	
	150 155 160	
35	AGT GTC CTG GCA TGG GTA ACA GCC ATT CTG GCC ACT TTG CCT GAA TTC	585
	Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Phe	
	165 170 175	
40	GTG GTT TAT AAA CCT CAG ATG GAA GAC CAG AAA TAC AAG TGT GCA TTT	633
	Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys Cys Ala Phe	
	180 185 190 195	
	AGC AGA ACT CCC TTC CTG CCA GCT GAT GAG ACA TTC TGG AAG CAT TTT	681
	Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp Lys His Phe	
	200 205 210	
45	CTG ACT TTA AAA ATG AAC ATT TCG GTT CTT GTC CTC CCC CTA TTT ATT	729
	Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro Leu Phe Ile	
	215 220 225	
50	TTT ACA TTT CTC TAT GTG CAA ATG AGA AAA ACA CTA AGG TTC AGG GAG	777
	Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe Arg Glu	
	230 235 240	
55	CAG AGG TAT AGC CTT TTC AAG CTT GTT TTT GCC GTA ATG GTA GTC TTC	825
	Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met Val Val Phe	
	245 250 255	
60	CTT CTG ATG TGG GCG CCC TAC AAT ATT GCA TTT TTC CTG TCC ACT TTC	873
	Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Leu Ser Thr Phe	
	260 265 270 275	

	AAA GAA CAC TTC TCC CTG AGT GAC TGC AAG AGC AGC TAC AAT CTG GAC	921
	Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp	
	280 285 290	
5	AAA AGT GTT CAC ATC ACT AAA CTC ATC GCC ACC ACC CAC TGC TGC ATC	969
	Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile	
	295 300 305	
10	AAC CCT CTC CTG TAT GCG TTT CTT GAT GGG ACA TTT AGC AAA TAC CTC	1017
	Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu	
	310 315 320	
15	TGC CGC TGT TTC CAT CTG CGT AGT AAC ACC CCA CTT CAA CCC AGG GGG	1065
	Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln Pro Arg Gly	
	325 330 335	
20	CAG TCT GCA CAA GGC ACA TCG AGG GAA GAA CCT GAC CAT TCC ACC GAA	1113
	Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu	
	340 345 350 355	
	GTG TAAACTAGCA TCCACCAAAT GCAAGAAGAA TAAACATGGA TTTTCATCTT	1166
	Val	
25	TCTGCATTAT TTCATGTAAA TTTTCTACAC ATTTGTATAC AAAATCGGAT ACAGGAAGAA	1226
	AAGGGAGAGG TGAGCTAACA TTTGCTAAGC ACTGAATTTG TCTCAGGCAC CGTGCAAGGC	1286
30	TCTTTACAAA CGTGAGCTCC TTCGCCTCCT ACCACTTGTC CATAGTGTGG ATAGGACTAG	1346
	TCTCATTTCT CTGAGAAGAA AACTAAGGCG CGGAAATTTG TCTAAGATCA CATAACTAGG	1406
	AAGTGGCAGA ACTGATTCTC CAGCCCTGGT AGCATTTGCT CAGAGCCTAC GCTTGGTCCA	1466
35	GAACATCAAA CTCCAAACCC TGGGGACAAA CGACATGAAA TAAATGTATT TTAAACATA	1526
	TAAAAAAAAA AAAAAAAAAA A	1547
40	(2) INFORMATION FOR SEQ ID NO:12:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 356 amino acids	
	(B) TYPE: amino acid	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
50	Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr	
	1 5 10 15	
55	Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu	
	20 25 30	
	Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu	
	35 40 45	
60	Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly	

	50	55	60
	Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly		
	65	70	75 80
5	Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn		
		85	90 95
	Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp		
10		100	105 110
	Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser		
		115	120 125
15	Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe		
		130 135	140
	Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly		
		145 150	155 160
20	Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu		
		165	170 175
	Pro Glu Phe Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys		
25		180	185 190
	Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp		
		195	200 205
30	Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro		
		210 215	220
	Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg		
		225 230	235 240
35	Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met		
		245	250 255
	Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu		
40		260	265 270
	Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr		
		275	280 285
45	Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His		
		290 295	300
	Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser		
		305 310	315 320
50	Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln		
		325	330 335
	Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His		
55		340	345 350
	Ser Thr Glu Val		
		355	

60 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

15 Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
1 5 10 15
20 Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
20 25 30
25 Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
35 40 45
30 Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
50 55 60
35 Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80
40 Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
85 90 95
45 Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
100 105 110
50 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125
55 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
130 135 140
60 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
145 150 155 160
65 Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
165 170 175
70 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
180 185 190
75 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
195 200 205
80 Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220
85 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
225 230 235 240
90 Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn

245 250 255

Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
260 265 270

5 Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
275 280 285

Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

10 Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
305 310 315 320

15 Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
325 330 335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser
340 345 350

20 Ala Gly Phe
355

(2) INFORMATION FOR SEQ ID NO:14:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40 Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
1 5 10 15

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
20 25 30

45 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
35 40 45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
50 55 60

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
65 70 75 80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
85 90 95

55 Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
100 105 110

60 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile

	115	120	125
	Phe Phe Ile Ile Leu Leu Thr	Ile Asp Arg Tyr Leu Ala Ile Val His	
	130	135	140
5	Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr		
	145	150	155 160
10	Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile		
	165	170	175
	Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro		
	180	185	190
15	Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile		
	195	200	205
	Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly		
	210	215	220
20	Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg		
	225	230	235 240
	Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp		
	245	250	255
25	Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe		
	260	265	270
30	Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln		
	275	280	285
	Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile		
	290	295	300
35	Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu		
	305	310	315 320
	Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly		
	325	330	335
40	Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp		
	340	345	350
45	Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu		
	355	360	365
	Gln Asp Lys Glu Gly Ala		
	370		

50

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

5 Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
 1 5 10 15
 10 Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
 20 20 25 30
 Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
 35 40 45
 15 Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
 50 55 60
 Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80
 20 Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
 85 90 95
 His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
 100 105 110
 25 Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
 115 120 125
 30 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
 130 135 140
 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
 145 150 155 160
 35 Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
 165 170 175
 Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
 180 185 190
 Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
 195 200 205
 45 Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220
 Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
 225 230 235 240
 50 Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
 245 250 255
 Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
 260 265 270
 55 Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
 275 280 285
 60 Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val

290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305 310 315 320

5 Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
325 330 335

10 Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
340 345 350

Ile Val Phe
355

15 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

30 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
20 25 30

35 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
35 40 45

40 Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65 70 75 80

45 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
85 90 95

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
100 105 110

50 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
115 120 125

55 Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160

60 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser

	165	170	175
	Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser		
	180	185	190
5	Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile		
	195	200	205
	Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met		
10	210	215	220
	Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala		
	225	230	235
15	Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr		
	245	250	255
	Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val		
	260	265	270
20	Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala		
	275	280	285
	Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr		
25	290	295	300
	Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys		
	305	310	315
30	Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln		
	325	330	335
	Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met		
	340	345	350
35	Asp His Asp Leu His Asp Ala Leu		
	355	360	

(2) INFORMATION FOR SEQ ID NO:17:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATGATCA GTCAACGGGG GAC

23

55

(2) INFORMATION FOR SEQ ID NO:18:

- 60 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10

CCAGCAAGCT TGCAACCTTA ACCA

24

(2) INFORMATION FOR SEQ ID NO:19:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Tyr Lys Asp Asp Asp Asp Lys Leu
1 5

30